

STIC-ILL

PP 501. M523

From: Wilder, Cynthia
Sent: Monday, March 01, 2004 5:00 PM
To: STIC-ILL
Subject: Reference request

Please provide the following:

Usui et al. Molecular and chemical neuropathology (neurochemistry and cerebrospinal fluid) (1991 Dec) vol. 15, No. 3, pages 207-216, ISSN: 1044-7393

Nagata et al. Journal of Histochemistry and Cytochemistry, (1992), vol. 40, No. 4, pages 591, ISSN: 0022-1554.

Stern et al. Journal of Pediatric surgery, (Jan 2001) vol. 36, No. 1, pages 190-195, ISSN: 0022-3468

thank you

Cynthia B. Wilder, Ph.D.
United States Patent and TradeMark Office
Carlisle Remson 2A35
Mailbox: 2C18
571/272-0791

(FILE 'HOME' ENTERED AT 15:54:57 ON 01 MAR 2004)

FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT' ENTERED
AT 15:55:33 ON 01 MAR 2004

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L1      31061 S ASAI S?/AU OR NAGATA T?/AU OR TAKAHASHI Y?/AU OR ISHIKAWA K?/  
L2      266 S L1 AND IN SITU HYBRIDIZATION  
L3      29 S L2 AND (LOCALIZATION AND MRNA)  
L4      14 DUP REM L3 (15 DUPLICATES REMOVED)  
L5      59 S IN SITU HYBRIDIZATION  
L6      15258 S INSITU HYBRIDIZATION  
L7      257067 S IN SITU HYBRIDIZATION  
L8      1449 S (L6 OR L7) AND (SCREEN### (5A) GENE#)  
L9      2 S L8 AND (LOCALIZATION (3A) MRNA)  
L10     73 S L8 AND (LOCALIZATION AND MRNA)  
L11     7 S L10 AND (DNA CHIP OR MICROCHIP OR MICROARRAY OR DNA MICROARRA  
L12     4 DUP REM L11 (3 DUPLICATES REMOVED)  
L13     387 S L8 AND MRNA  
L14     28 S L13 AND (DNA CHIP OR MICROCHIP OR MICROARRA OR CHIP OR ARRAY)  
L15     20 DUP REM L14 (8 DUPLICATES REMOVED)  
L16     38 DUP REM L10 (35 DUPLICATES REMOVED)
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=> s l13 and l7

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L17      383 L13 AND L7
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=> s l17 and probe

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L18      63 L17 AND PROBE
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=> s dup rem l18

MISSING OPERATOR REM L18

The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> dup rem l18

PROCESSING COMPLETED FOR L18

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L19      42 DUP REM L18 (21 DUPLICATES REMOVED)
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=> s l19 and localiz?

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L20      12 L19 AND LOCALIZ?
```

=> dup rem l120

L120 IS NOT VALID HERE

The L-number entered has not been defined in this session, or it
has been deleted. To see the L-numbers currently defined in this
session, enter DISPLAY HISTORY at an arrow prompt (=>).

=> dup rem l20 1-12

'1-12' IS NOT VALID. VALID FILE NAMES ARE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS'
You have entered a file name of duplicates to keep that is not
referenced by any of the L#s specified for this DUPLICATE command.
The file names of duplicates that can be kept are listed above.
Please enter one of these file names.

=> dup rem l20

PROCESSING COMPLETED FOR L20

```
L21      12 DUP REM L20 (0 DUPLICATES REMOVED)
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=> d ibib abs l21 1-12

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L21 ANSWER 1 OF 12 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.  
on STN
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ACCESSION NUMBER: 2003330687 EMBASE

TITLE: Global gene profiling analysis of mouse uterus during the
oestrous cycle.

AUTHOR: Tan Y.F.; Li F.X.; Piao Y.S.; Sun X.Y.; Wang Y.L.

CORPORATE SOURCE: Y.L. Wang, State Key Lab. Reproductive Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing 100080, China. wangyl@panda.ioz.ac.cn

SOURCE: Reproduction, (1 Aug 2003) 126/2 (171-182).
 Refs: 53
 ISSN: 1470-1626 CODEN: RCUKBS

COUNTRY: United Kingdom

DOCUMENT TYPE: Journal; General Review

FILE SEGMENT: 003 Endocrinology
 021 Developmental Biology and Teratology
 029 Clinical Biochemistry

LANGUAGE: English

SUMMARY LANGUAGE: English

AB Many genes related to the cyclic changes of the uterus during the oestrous cycle have been identified using a one-by-one approach. In the present study, cDNA microarray technology was applied to investigate the global profile of gene expression of mouse uterus at the oestrous and dioestrous stages. At a certain stage of the oestrous cycle, the uteri of mature CD-1 mice (n = 10) were removed, pooled and snap-frozen in liquid nitrogen. Total RNA was extracted to synthesize cDNA probes for microarray assay. By **screening** 8192 mouse **genes** and expressed sequence tags (ESTs), 51 upregulated and 51 downregulated genes were identified in oestrous uterus, of which 62 are well characterized and 40 are ESTs. The known genes were assigned to various gene categories according to their main function. The microarray was performed three times with three independent sets of uterine tissue pools. The results of northern blot analysis for small proline-rich protein 2 (Sprr2), 17 β -hydroxysteroid dehydrogenase type 2 (17 β HSD-2), high mobility group 2 (Hmg2), mitotic checkpoint component 2 (Mad2) and an EST AW555366 **mRNA** were consistent with that of microarray analysis. In **situ hybridization** was performed to **localize** the transcript of the EST AW555366. Most of the upregulated genes encode secreted immune-related proteins, proteinases and their inhibitors, indicating their potential involvement in sperm viability as well as capacitation. The downregulated genes mainly encode cell cycle-related factors, implying the active proliferation of uterus at dioestrus.

L21 ANSWER 2 OF 12 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN

ACCESSION NUMBER: 2002-14126 BIOTECHDS

TITLE: Novel peptide designated as human kinase useful as target for diagnosing a disease or predisposition to the disease mediated by the peptide;
 vector-mediated gene transfer, expression in host cell and antibody for recombinant protein production, drug **screening** and **gene** therapy

AUTHOR: BEASLEY E M; WEI M; BONAZZI V R; SANDERS R; DI FRANCESCO V

PATENT ASSIGNEE: PE CORP NY

PATENT INFO: WO 2002024920 28 Mar 2002

APPLICATION INFO: WO 2000-US29161 19 Sep 2000

PRIORITY INFO: US 2000-729995 6 Dec 2000

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2002-404955 [43]

AN 2002-14126 BIOTECHDS

AB DERWENT ABSTRACT:

NOVELTY - An isolated peptide designated human kinase (HK) consisting or comprising of an amino acids sequence (S1) containing 505 amino acids fully defined in the specification, its allelic variant, ortholog or fragment, is new.

DETAILED DESCRIPTION - HK comprises (S1), its ortholog, variant or fragment, each comprising (S1), where the variant or ortholog is encoded by a nucleic acid molecule that hybridizes under stringent conditions to the opposite strand of the nucleic acid molecule comprising a sequence (S2) of 2190 or 29629 base pairs fully defined in the specification, or

the fragment comprises 10 contiguous amino acids. INDEPENDENT CLAIMS are included for the following: (1) an isolated antibody (Ab) that binds to HK; (2) an isolated nucleic acid molecule (NA) consisting and/or comprising a nucleotide sequence from the same which encodes (S1), its variant ortholog, and fragment, each encoded by (S1) where the variant and ortholog are encoded by (S2), the fragment comprising 10 contiguous amino acids and the complement of the nucleotide sequence; (3) a gene chip comprising NA; (4) a transgenic non-human animal (NHA) comprising NA; (5) a nucleic acid vector (V) comprising NA; (6) a host cell (HC) containing (V); (7) producing HK; (8) a pharmaceutical composition (PC) comprising an agent identified by contacting HK with it and assaying the mixture to determine whether a complex is formed with the agent bound to the peptide; (9) an isolated human kinase peptide having a sequence 70% identical to (S1); (10) an isolated nucleic acid molecule encoding a human kinase peptide having 80% homology with (S2); (11) detecting the presence of HK in a sample involving contacting the sample with a detection agent that specifically allows detection of the presence of HK in the sample and then detecting the presence of HK; and (12) detecting the presence of NA in a sample involving contacting the sample with an oligonucleotide that hybridizes to NA under stringent conditions and determining whether oligonucleotide binds to NA in the sample.

WIDER DISCLOSURE - The following are disclosed: (1) kits for using antibodies to detect the presence of a protein in a biological sample, detecting the presence of kinase nucleic acid in a biological sample; and (2) nucleic acid detection kits, such as arrays or microarrays of nucleic acid molecules that are based on the sequence information provided in (S2).

BIOTECHNOLOGY - Preparation: Producing HK involves introducing a nucleotide sequence encoding (S1) into HC, and culturing HC under conditions in which the peptides (HK) are expressed from the nucleotide sequence (claimed). Preferred Peptide: HK shares 90% homology with (S1). Preferred Nucleic Acid: NA shares 90% homology with (S2).

ACTIVITY - None given.

MECHANISM OF ACTION - Kinase modulator. No supporting data is given.

USE - HK is useful for identifying a modulator of it, by contacting HK with an agent and determining if the agent has modulated the function, expression or activity of HK, where the agent is administered to HC comprising an expression vector that expresses HK. HK is also useful for identifying an agent that binds to any of the peptides involving contacting HK with an agent and assaying the contacted mixture to determine whether a complex is formed with the agent bound to HK. PC is useful for treating a disease, or condition mediated by HK (claimed). HK is useful to screen a compound for the ability to stimulate or inhibit interaction between HK and molecule that normally interacts with HK. HK is useful as bait proteins in a 2 or 3 hybrid assays to identify other proteins, which bind or interact with HK and are involved in HK activity. HK is also useful to provide a target for diagnosing a disease or predisposition to disease mediated by HK and also useful in pharmacogenetic analysis. HK is also useful for treating a disorder characterized by absence of inappropriate or unwanted expression of HK, also as an immunogen to raise Ab by administering HK to a mammalian organism e.g. rat, rabbit or mouse. Ab is useful to isolate HK by affinity chromatography or immuno precipitation and also to detect protein in situ in vitro or in a cell lysate or supernatant in order to evaluate the abundance and pattern of expression. Ab is also useful to assess normal and aberrant subcellular localization of cells in various tissues in an organism. Ab is also useful in pharmacogenomic analysis and also useful as diagnostic tools as an immunological marker for aberrant protein analyzed by electrophoretic mobility, isoelectric point, tryptic peptide digest and other physical assays. Ab is further useful in tissue typing where a specific protein has been correlated with expression in specific tissue, antibodies that are specific for this protein which can be useful to identify a tissue type. NA is useful as a hybridization probes for mRNA, transcript/cDNA and genomic DNA to isolate

full length cDNA and genomic clones encoding the peptide and to isolate cDNA and genomic clones that corresponds to variants producing the same or related peptides, to synthesize antisense molecules of desired length and sequence and also useful as probes for determining the chromosomal positions of it by means of **in situ hybridization** methods. NA is useful in making vectors containing the gene regions of NA, for designing ribozymes corresponding to all or a part of **mRNA** produced from NA, for constructing HC and also for constructing transgenic animals expressing NA and peptides. NA is also useful as hybridization probes for determining the presence level, form and distribution of NA expression, for monitoring the effectiveness of modulating compounds on the expression or activity of HK gene in clinical trials or in treatment regimen and also useful as antisense constructs to control kinase gene expression in cells, tissues and organisms. HC is useful for HK production and also useful for conducting cell-based assays involving the HK or its fragments. Recombinant HC expressing a native HK is useful for assaying compounds that stimulate or inhibit HK function. HC are also useful for identifying HK mutants in which these functions are affected. Genetically engineered HC are useful to produce NHA, e.g. rodent such as rat or mouse in which one or more of the cells of the animal include a transgene.

EXAMPLE - None given. (90 pages)

L21 ANSWER 3 OF 12 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
 ACCESSION NUMBER: 2003-16287 BIOTECHDS

TITLE: **Screening of a gene, and monitoring of**
 gene expression comprises in **situ**
hybridization techniques;
 gene expression analysis in cerebral anemia mouse animal
 model

PATENT ASSIGNEE: UNIV NIPPON
 PATENT INFO: JP 2002306174 22 Oct 2002
 APPLICATION INFO: JP 2001-112367 11 Apr 2001
 PRIORITY INFO: JP 2001-112367 11 Apr 2001; JP 2001-112367 11 Apr 2001
 DOCUMENT TYPE: Patent
 LANGUAGE: Japanese
 OTHER SOURCE: WPI: 2003-423960 [40]
 AN 2003-16287 BIOTECHDS
 AB DERWENT ABSTRACT:

NOVELTY - **Screening** a **gene** in which a **probe**
 hybridizing specifically with an **mRNA** and/or an expression gene
 sequence fragment, which are expression products of a gene used to carry
 out an **in situ hybridization** of a biotissue or a cell
 sample, and to investigate **localization** of **mRNA**
 and/or expression gene sequence fragment in tissue or cell.

DETAILED DESCRIPTION - A method for monitoring gene expression in
 which a tissue or a cell sample are respectively collected from a living
 body before and after a phenomenon occurs, and the samples are **in situ**
 hybridized by using the above **probe** to investigate
localization of said **mRNA** and/or expression gene
 sequence fragment in said tissue or said cell.

USE - The method is used for **screening a gene**
 and monitoring **gene** expression.

EXAMPLE - Both side total carotid arteries of mature mice were
 ligated for 20 minutes to interrupt blood current and to give cerebral
 anemia models. The blood current was entrestored, the mice were killed
 periodically and the hippocampi were taken and the gene expression was
 analyzed. (22 pages)

L21 ANSWER 4 OF 12 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 ACCESSION NUMBER: 2002:287091 BIOSIS
 DOCUMENT NUMBER: PREV200200287091
 TITLE: Plunc, a member of the secretory gland protein family, is
 up-regulated in nasal respiratory epithelium after

olfactory bulbectomy.
AUTHOR(S): Sung, Young K.; Moon, Cheil; Yoo, Joo-yeon; Moon, Chanil;
Pearse, David; Pevsner, Jonathan; Ronnett, Gabriele V.
[Reprint author]
CORPORATE SOURCE: Dept. of Neuroscience, Johns Hopkins University School of
Medicine, 725 N. Wolfe St., PCTB 1006B, Baltimore, MD,
21205, USA
gronnett@jhmi.edu
SOURCE: Journal of Biological Chemistry, (April 12, 2002) Vol. 277,
No. 15, pp. 12762-12769. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 8 May 2002
Last Updated on STN: 8 May 2002

AB Subtraction suppression hybridization was used with high throughput
screening to identify transcripts of **genes** that are
differentially expressed in nasal epithelium following lesioning of the
olfactory bulb, termed bulbectomy. We isolated the rat homologue of
plunc, a murine gene highly expressed in lung and nasopharyngeal regions,
by this method. Rat plunc encodes a 270-amino acid protein containing a
putative signal peptide. plunc up-regulation in respiratory epithelium was
confirmed by Northern blot and in **situ hybridization**.
plunc mRNA was expressed in nasal epithelium, heart, lung,
thymus, and salivary gland in adult rodent. plunc was expressed in nasal
epithelium, thymus, and salivary gland during embryogenesis. Antibodies
against Plunc detected a 31-kDa protein in lung, heart, and spleen. Rat
nasal epithelium displayed robust immunoreactivity that was highly
localized to the microvilli layer of respiratory epithelium. The
expression of plunc was up-regulated after bulbectomy in respiratory
epithelium. We also detected secreted plunc in rat and human mucus.
Sequence and homology analyses suggest that Plunc is a member of the
secretory gland protein family with putative bactericidal/bacteriostatic
function. This is the first protein found in respiratory epithelium whose
expression is regulated by olfactory neuronal injury and may provide
protection against infection subsequent to injury.

L21 ANSWER 5 OF 12 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2001:329877 BIOSIS
DOCUMENT NUMBER: PREV200100329877
TITLE: Neuronal expression of synaptotagmin-related gene 1 is
regulated by thyroid hormone during cerebellar development.
AUTHOR(S): Potter, Gregory B.; Facchinetti, Fabrizio; Beaudoin, Gerard
M. J., III; Thompson, Catherine C. [Reprint author]
CORPORATE SOURCE: Kennedy Krieger Research Institute, 707 North Broadway, 4th
floor, Baltimore, MD, 21205, USA
thompsonc@kennedykrieger.org
SOURCE: Journal of Neuroscience, (June 15, 2001) Vol. 21, No. 12,
pp. 4373-4380. print.
CODEN: JNRSDS. ISSN: 0270-6474.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 11 Jul 2001
Last Updated on STN: 19 Feb 2002

AB Thyroid hormone (TH) is essential for proper brain development, acting
through nuclear receptors that modulate the expression of specific genes
in response to hormone binding. In a **screen** for **genes**
regulated by TH in the rat cerebellum, we recently identified a novel
gene, synaptotagmin-related gene 1 (Srg1). The Srg1 protein is
structurally similar to synaptotagmins, a family of proteins involved in
regulating neurotransmission. To elucidate a potential role of Srg1 in
brain development, we have investigated the developmental and TH-regulated
expression of Srg1 in the neonatal rat brain. We show that expression of
both Srg1 RNA and protein is detected only in the brain and specifically

in neurons. Srg1 mRNA and protein levels increase postnatally, nearing adult levels after the third postnatal week. Neonatal TH deficiency results in a significant reduction and delay in expression of both Srg1 RNA and protein. Using immunohistochemistry, we were able to detect Srg1 protein in numerous brain regions. In the cerebellum, Srg1 protein is **localized** to the molecular layer, indicating that it is highly expressed in granule cell axons. To further examine Srg1 expression in cerebellar granule cells (CGCs), we used an in vitro cell culture model. In primary cultures of CGCs, Srg1 expression is significantly reduced in the absence of TH. Srg1 mRNA is rapidly upregulated in cultured CGCs, suggesting a direct response to TH. Neuronal and TH-regulated expression of Srg1, together with its **localization** to neurites, implicates Srg1 as an important component of the program of gene expression induced by TH in the developing brain.

L21 ANSWER 6 OF 12 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 ACCESSION NUMBER: 2002:210665 BIOSIS
 DOCUMENT NUMBER: PREV200200210665
 TITLE: Chromosomal distribution, **localization** and expression of the human endogenous retrovirus ERV9.
 AUTHOR(S): Svensson, A.-C.; Raudsepp, T.; Larsson, C.; Di Cristofano, A.; Chowdhary, B.; La Mantia, G.; Rask, L.; Andersson, G. [Reprint author]
 CORPORATE SOURCE: Department of Animal Breeding and Genetics, Upsala Biomedical Center, Swedish University of Agricultural Sciences, S-751 24, Upsala, Sweden
 SOURCE: Goran.Andersson@bmc.uu.se
 Cytogenetics and Cell Genetics, (2001) Vol. 92, No. 1-2, pp. 89-96. print.
 CODEN: CGCGBR. ISSN: 0301-0171.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 ENTRY DATE: Entered STN: 27 Mar 2002
 Last Updated on STN: 27 Mar 2002

AB ERV9 is a class I family of human endogenous retroviral sequences. Somatic cell hybrid genomic hybridization experiments using a mono-chromosomal panel indicate the presence of approximately 120 ERV9 loci in the human genome distributed on most chromosomes. Fluorescence in **situ hybridization** (FISH) using an ERV9 cDNA **probe** containing gag, pol and env sequences, verified this observation and a consistent signal was found at the chromosome region 11q13.3 fwdarw q13.5. By analysis of a panel of radiation hybrids, an ERV9 locus was mapped to within a 300-kbp region at the chromosome site 11q13. The marker CCLGW567 and the locus MAP3K11/D11S546 centromeric and telomeric flanked it, respectively. Northern blot analysis, using an ERV9 LTR **probe**, indicated that most normal tissues examined expressed low abundant ERV9 LTR driven mRNAs of various sizes. The most prominent expression was found in adrenal glands and testis. However, the level of expression varied in the same tissues among different individuals indicating that ERV9 mRNA expression probably is inducible in certain tissues or at various cell stages.

L21 ANSWER 7 OF 12 MEDLINE on STN
 ACCESSION NUMBER: 2000122160 MEDLINE
 DOCUMENT NUMBER: PubMed ID: 10656923
 TITLE: Coding sequence, chromosomal **localization**, and expression pattern of Nrfl: the mouse homolog of Drosophila erect wing.
 AUTHOR: Schaefer L; Engman H; Miller J B
 CORPORATE SOURCE: Myogenesis Research Laboratory, Massachusetts General Hospital, Charlestown 02129, USA.
 SOURCE: Mammalian genome : official journal of the International Mammalian Genome Society, (2000 Feb) 11 (2) 104-10.

PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000309
Last Updated on STN: 20000309
Entered Medline: 20000218

AB In *Drosophila*, the erect wing (ewg) protein is required for proper development of the central nervous system and the indirect flight muscles. The fly ewg gene encodes a novel DNA-binding domain that is also found in four genes previously identified in sea urchin, chicken, zebrafish, and human. To identify mouse ewg homologs, we designed degenerate primers to the conserved DNA-binding domain. The RT-PCR product obtained from **mRNA** of the mouse muscle cell line C2C12 was used to **screen** cDNA libraries; a single **gene** was identified which encodes a predicted 503 amino acid protein. The mouse ewg homolog, termed Nrfl, was mapped to proximal Chr 6. By RT-PCR and Northern analysis, Nrfl was expressed in all tissues examined, and Northern analysis on adult tissues revealed a complex banding pattern suggesting extensive alternative splicing. Nrfl hybridized to **mRNA** transcripts at approximately 2.2 kb, 4.0 kb, 4.4 kb, and 5.0 kb, with additional tissue-specific transcripts at 1.5 kb in testis, 1.9 kb in lung, and 3.7 kb in skeletal muscle. In **situ hybridization** on whole-mount E9-10.5 embryos showed a broad pattern of expression, with the highest levels of expression in the central nervous system, somites, first branchial arch, optic vesicle, and otic vesicle.

L21 ANSWER 8 OF 12 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 1998086331 EMBASE
TITLE: A new human homeobox gene OG12X is a member of the most conserved homeobox gene family and is expressed during heart development in mouse.
AUTHOR: Semina E.V.; Reiter R.S.; Murray J.C.
CORPORATE SOURCE: J.C. Murray, Department of Pediatrics, The University of Iowa, 200 Hawkins Drive, W229-1 GH, Iowa City, IA 52242, United States. jeff-murray@uiowa.edu
SOURCE: Human Molecular Genetics, (1998) 7/3 (415-422).

Refs: 46
ISSN: 0964-6906 CODEN: HMGEE5
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 021 Developmental Biology and Teratology
022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Homeodomain (HD) proteins are transcription regulators controlling a variety of cell fates. The HD region characterizing this protein family is a domain of 60 amino acid residues that recognizes and binds a site in the regulatory region of the target gene. It has been suggested that regions outside the HD may determine the specific functions of the various HD proteins by forming additional contacts with DNA sequences or by interactions with other proteins. We have identified a 14 amino acid motif within the C-terminal region of the protein encoded by the RIEG1 gene that is conserved among several HD proteins. Overlapping expression of the genes encoding these proteins during craniofacial development suggested that they might interact with a common factor. In order to identify additional **genes** possessing this motif we **screened** a human craniofacial cDNA library with oligoprobes. A novel gene was identified, exhibiting the most homology to murine Ogl2x (formerly OG12) and the recently reported human SHOX gene. Human OG12X and murine Ogl2x

L4 ANSWER 14 OF 14 MEDLINE on STN DUPLICATE 7

ACCESSION NUMBER: 92222507 MEDLINE

DOCUMENT NUMBER: PubMed ID: 1807267

TITLE: In **situ hybridization** histochemistry of
Spot 35 protein, a calcium-binding protein, in the rat
brain.

AUTHOR: Usui H; Katagiri T; Yoshida Y; Nishiyama A; Ichikawa T;
Kuвано R; **Takahashi Y**; Kumanishi T

CORPORATE SOURCE: Department of Neuropathology, Niigata University, Japan.

SOURCE: Molecular and chemical neuropathology / sponsored by the
International Society for Neurochemistry and the World
Federation of Neurology and research groups on
neurochemistry and cerebrospinal fluid, (1991 Dec) 15 (3)
207-16.
Journal code: 8910358. ISSN: 1044-7393.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199205

ENTRY DATE: Entered STN: 19920607
Last Updated on STN: 19920607
Entered Medline: 19920518

AB Using in **situ hybridization**, we analyzed the
localization of **mRNA** for Spot 35 protein (Spot 35), a
calcium-binding protein of the EF-hand type, in the rat cerebellum at
various developmental stages. A cDNA fragment corresponding to part of
the 3'-noncoding region was 35S-labeled and used as a hybridization probe.
Autoradiographic signals for Spot 35 **mRNA** were detected in all
the Purkinje cells, but not in any other neurons or glial cells in the
adult rat cerebellum. There was no significant difference in signal
intensity among individual cells. The signals were observed exclusively
in Purkinje cell bodies, but not in their processes, in striking contrast
to previous immunohistochemical studies in which Spot 35 protein was
demonstrated in both cell bodies and processes. In the time-course study,
signals for Spot 35 **mRNA** were detected in Purkinje cell bodies
weakly at embryonic day 19, thereafter more intensely at more developed
stages and most intensely at postnatal days 30 and 60 (adulthood). The
signal intensities of individual cells were similar at each of these
developmental stages except for the very early stages at which signals
were weak and slightly variable among cells. These findings, especially
that of the characteristic coordinated expression of Spot 35 **mRNA**
at given stages, should prove useful in studies of degenerative diseases
in the cerebellum in experimental animals and man. A weak expression of
Spot 35 **mRNA** in some of non-Purkinje cells was also noted.

=>

PubMed ID: 11528203

TITLE: High-throughput microarray technologies: from genomics to clinics.
AUTHOR: Bubendorf L
CORPORATE SOURCE: Institute for Pathology, University of Basel, Switzerland..
lbubendo@bluewin.ch
SOURCE: European urology, (2001 Aug) 40 (2) 231-8. Ref: 28
Journal code: 7512719. ISSN: 0302-2838.
PUB. COUNTRY: Switzerland
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200207
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20020716
Entered Medline: 20020715

characterization of the ribosomal gene **array**. Here we describe the cloning, sequencing, and confirmation, by fluorescence in **situ hybridization**, of the 18S rDNA gene, a region which includes the end of the 18S rDNA gene, an internal transcribed spacer, and a portion of the 5' end of the 28S rDNA gene in *H. chrysoscelis*.

L15 ANSWER 18 OF 20 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 2001209777 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11298187
TITLE: Subtractive hybridization--genetic takeaways and the search for meaning.
AUTHOR: Byers R J; Hoyland J A; Dixon J; Freemont A J
CORPORATE SOURCE: Laboratory Medicine Academic Group, University of Manchester, Manchester, UK.. r.byers@man.ac.uk
SOURCE: International journal of experimental pathology, (2000 Dec) 81 (6) 391-404. Ref: 113
Journal code: 9014042. ISSN: 0959-9673.
PUB. COUNTRY: England: United Kingdom

PubMed ID: 11150463

TITLE: cDNA microarray analysis of adapting bowel after intestinal resection.
AUTHOR: Stern L E; Erwin C R; Falcone R A; Huang F S; Kemp C J; Williams J L; Warner B W
CORPORATE SOURCE: Division of Pediatric Surgery, Children's Hospital Medical Center, Department of Surgery, University of Cincinnati College of Medicine, Cincinnati, OH 45229-3039, USA.
CONTRACT NUMBER: F32 DK09882 (NIDDK)
RO-1 DK53234 (NIDDK)
SOURCE: Journal of pediatric surgery, (2001 Jan) 36 (1) 190-5.
Journal code: 0052631. ISSN: 0022-3468.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010604
Last Updated on STN: 20010604
Entered Medline: 20010531

AB BACKGROUND/PURPOSE: Studies of the genetic regulation of various physiologic processes have been hampered by methodologies that are limited to the analysis of individual genes. The advent of cDNA microarray technology has permitted the simultaneous **screening** of numerous **genes** for alterations in expression. In this study, cDNA microarrays were used to evaluate gene expression changes during the intestinal adaptive response to massive small bowel resection (SBR). METHODS: Male ICR mice (n = 20) underwent either a 50% SBR or sham operation and then were given either orogastric epidermal growth factor (EGF, 50 microg/kg/d) or saline. After 3 days, cDNA microarray analysis was performed on **mRNA** extracted from the remnant ileum. RESULTS: From over 8,700 different genes, the **array** identified 27 genes that were altered 2-fold or greater after SBR. Small proline-rich protein 2 (sprr2), the gene with the greatest expression change (4.9-fold), was further upregulated by EGF. This gene has never been characterized in the intestine or described in intestinal adaptation. CONCLUSIONS: cDNA microarray analysis showed enhanced expression of sprr2, a gene not previously known to be involved in the physiology of adaptation after SBR. This technology provides a more rapid and efficient means of dissecting the complex genetic regulation of gut adaptation.

L15 ANSWER 17 OF 20 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 2002:210669 BIOSIS
DOCUMENT NUMBER: PREV200200210669
TITLE: Cloning of the 18S rDNA gene, an internal transcribed spacer, and the 5' region of the 28S rDNA gene of Cope's gray treefrog, *Hyla chrysoscelis*.
AUTHOR(S): Owens, G., Jr.; Wiley, J. E. [Reprint author]
CORPORATE SOURCE: Department of Pediatrics, The Brody School of Medicine, East Carolina University, Greenville, NC, 27858, USA
wileyj@mail.ecu.edu
SOURCE: Cytogenetics and Cell Genetics, (2001) Vol. 92, No. 1-2, pp. 111-115. print.
CODEN: CGCGBR. ISSN: 0301-0171.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 27 Mar 2002
Last Updated on STN: 27 Mar 2002

AB The location of rDNA genes on the chromosomes of most species is identical within that species, usually occurring on the same chromosome or chromosomes. This is not the case in Cope's gray treefrog, *Hyla chrysoscelis*, where the rDNA genes are polymorphic for chromosome location. The occasions leading to this polymorphism have yet to be determined. The first step in understanding the nature of the polymorphism is the

2003453051 EMBASE

TITLE: Distribution of α - and γ -synucleins in the adult rat brain and their modification by high-dose cocaine treatment.

AUTHOR: Brenz Verca M.S.; Bahi A.; Boyer F.; Wagner G.C.; Dreyer J.-L.

CORPORATE SOURCE: Dr. J.-L. Dreyer, Institute of Biochemistry, University of Fribourg, CH-1700 Fribourg, Germany. jean-luc.dreyer@unifr.ch

SOURCE: European Journal of Neuroscience, (2003) 18/7 (1923-1938). Refs: 55
ISSN: 0953-816X CODEN: EJONEI

COUNTRY: United Kingdom

DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 008 Neurology and Neurosurgery
037 Drug Literature Index
052 Toxicology

LANGUAGE: English

SUMMARY LANGUAGE: English

AB Synucleins have attracted much attention because of their involvement in several neurodegenerative disorders. In a **screening** for **genes** differentially expressed after high-dose cocaine exposure, we found γ -synuclein as a major upregulated candidate in the tegmentum. Overexpression of both α - and γ -synuclein after drug treatment was confirmed by means of microarrays, yielding an increase in the hippocampus, the striatum and the tegmentum (2.65 x, 1.96 x and 3.5 x, respectively, for α -synuclein vs. 2.7 x, 1.96 x and 7.16 x for γ -synuclein), but no change in the nucleus accumbens. Investigation of the distribution of **mRNA** (by **in situ hybridization**) and of the proteins (by immunocytochemistry) shows in both cases a clearly distinct pattern of expression for α - and γ -synuclein. α -synuclein displays a very characteristic distribution, confined to specific nuclei, whereas γ -synuclein is more widely expressed throughout the brain. **mRNA** of both α - and γ -synucleins display a complementary pattern of expression all over the cortex. In contrast to γ -synuclein, α -synuclein is neuronal, being only found in NeuN-expressing cells, and is expressed in the basal ganglia (faintly) and in the substantia nigra compacta where it is highly correlated with tyrosine hydroxylase. Immunocytochemistry shows that γ -synuclein generally colocalizes with glial fibrillary acidic protein-expressing cells and is abundant in the red nucleus, the substantia nigra reticulata and the anterior commissure, while γ -synuclein **mRNA** labels the matrix compartments of the caudate-putamen. The role of synucleins in relation to cocaine-induced plasticity or neurotoxicity is discussed.

L12 ANSWER 2 OF 4 MEDLINE on STN DUPLICATE 1

ACCESSION NUMBER: 2003239107 MEDLINE

DOCUMENT NUMBER: PubMed ID: 12761244

TITLE: AngRem104, an angiotensin II-induced novel upregulated gene in human mesangial cells, is potentially involved in the regulation of fibronectin expression.

AUTHOR: Liang Xiubin; Zhang Hong; Zhou Anyu; Wang Haiyan

CORPORATE SOURCE: Renal Division of Peking University First Hospital, Institute of Nephrology, Peking University, Beijing, China.

SOURCE: Journal of the American Society of Nephrology : JASN, (2003 Jun) 14 (6) 1443-51.
Journal code: 9013836. ISSN: 1046-6673.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF367870

ENTRY MONTH: 200308

ENTRY DATE: Entered STN: 20030523
Last Updated on STN: 20030821
Entered Medline: 20030820

AB Accumulation of extracellular matrix (ECM) in the glomerular mesangium is a common feature of many progressive renal diseases. Angiotensin II (AngII) plays important roles in the proliferation of glomerular mesangial cells (MC) as well as the synthesis of ECM such as fibronectin (FN) and collagens. However, the precise molecular signals responsible for these effects are unknown. To explore possible molecule mechanism of ECM accumulation related to AngII, suppression subtractive hybridization (SSH) was performed to **screen** and identify upregulated **genes** induced by AngII in cultured human MC. A novel gene, AngRem104 (GenBank accession number, AF367870), was isolated. The full-length cDNA of AngRem104 is 1690 bp, and it contains a 1041-bp open reading frame (ORF) encoding 347 amino acid residues with a predicted molecular mass of 37.2 kD. AngRem104 widely expressed in human heart, placenta, liver, muscle, kidney, and pancreas. Moreover, AngRem104 was found in human glomeruli and tubule by **in situ hybridization**. In human MC, the upregulation of AngRem104 induced by AngII was time-dependent, and it was dose-dependently blocked by AngII type 1 receptor antagonist (AT1RA), Losartan. The subcellular **localization** detected by AngRem104-pEGFP fusion protein revealed that AngRem104 was a nuclear protein. Interestingly, when AngRem104 was overexpressed by transfection of its sense construct, cDNA **Microarray** showed that two of the ECM-related genes, i.e., human **mRNA** for FN and integrin-beta-1 (FN receptor), dramatically upregulated their expressions. Furthermore, AngRem104 could regulate the expression of FN induced by AngII, which were detected by RT-PCR and quantitative real-time PCR, when AngRem104 was overexpressed. It is concluded that AngRem104 is a novel human gene potentially involved in the regulation of FN induced by AngII in human MC. These findings may provide new insights into mechanisms of glomerular sclerosis associated with AngII.

L12 ANSWER 3 OF 4 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 2003330687 EMBASE
TITLE: Global gene profiling analysis of mouse uterus during the oestrous cycle.
AUTHOR: Tan Y.F.; Li F.X.; Piao Y.S.; Sun X.Y.; Wang Y.L.
CORPORATE SOURCE: Y.L. Wang, State Key Lab. Reproductive Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing 100080, China. wangyl@panda.ioz.ac.cn
SOURCE: Reproduction, (1 Aug 2003) 126/2 (171-182).
Refs: 53
ISSN: 1470-1626 CODEN: RCUKBS
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 003 Endocrinology
021 Developmental Biology and Teratology
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Many genes related to the cyclic changes of the uterus during the oestrous cycle have been identified using a one-by-one approach. In the present study, cDNA **microarray** technology was applied to investigate the global profile of gene expression of mouse uterus at the oestrous and dioestrous stages. At a certain stage of the oestrous cycle, the uteri of mature CD-1 mice (n = 10) were removed, pooled and snap-frozen in liquid nitrogen. Total RNA was extracted to synthesize cDNA probes for **microarray** assay. By **screening** 8192 mouse **genes** and expressed sequence tags (ESTs), 51 upregulated and 51 downregulated genes were identified in oestrous uterus, of which 62 are well characterized and 40 are ESTs. The known genes were assigned to various gene categories according to their main function. The **microarray**

was performed three times with three independent sets of uterine tissue pools. The results of northern blot analysis for small proline-rich protein 2 (Sprr2), 17 β -hydroxysteroid dehydrogenase type 2 (17 β HSD-2), high mobility group 2 (Hmg2), mitotic checkpoint component 2 (Mad2) and an EST AW555366 mRNA were consistent with that of **microarray** analysis. In **situ hybridization** was performed to localize the transcript of the EST AW555366. Most of the upregulated genes encode secreted immune-related proteins, proteinases and their inhibitors, indicating their potential involvement in sperm viability as well as capacitation. The downregulated genes mainly encode cell cycle-related factors, implying the active proliferation of uterus at dioestrus.

Host gene regulation during coxsackievirus B3 infection in

mice: assessment by microarrays.

AUTHOR: Taylor L A; Carthy C M; Yang D; Saad K; Wong D; Schreiner G; Stanton L W; McManus B M

CORPORATE SOURCE: Department of Pathology and Laboratory Medicine, University of British Columbia, St. Paul's Hospital, Vancouver, Canada.

SOURCE: Circulation research, (2000 Aug 18) 87 (4) 328-34.
Journal code: 0047103. ISSN: 0009-7330.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200009

ENTRY DATE: Entered STN: 20000922

Last Updated on STN: 20000922

Entered Medline: 20000912

AB Host genetic responses that characterize enteroviral myocarditis have not yet been determined. The injurious and inflammatory process in heart muscle may reflect host responses of benefit to the virus and ultimately result in congestive heart failure and dilated cardiomyopathy. On the other hand, host responses within the myocardium may secure the host against acute or protracted damage. To investigate the nature of modified gene expression in comparison with normal tissue, **mRNA** species were assessed in myocardium using cDNA microarray technology at days 3, 9, and 30 after infection. Of 7000 clones initially **screened**, 169 known **genes** had a level of expression significantly different at 1 or more postinfection time points as compared with baseline. The known regulated genes were sorted according to their functional groups and normalized expression patterns and, subsequently, interpreted in the context of viremic, inflammatory, and healing phases of the myocarditic process.

Neuron-specific enolase (NSE) and non-neuronal enolase (NNE) mRNAs are co-expressed in neurons of the rat cerebellum: **in situ hybridization** histochemistry.

AUTHOR: Katagiri T; Feng X; Ichikawa T; Usui H; **Takahashi Y**; Kumanishi T

CORPORATE SOURCE: Department of Neuropathology, Niigata University, Japan.

SOURCE: Brain research. Molecular brain research, (1993 Jul) 19 (1-2) 1-8.

Journal code: 8908640. ISSN: 0169-328X.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199309

ENTRY DATE: Entered STN: 19931015
Last Updated on STN: 19970203
Entered Medline: 19930930

AB Using **in situ hybridization** histochemistry, we analysed the **localization** of mRNAs for neuron-specific enolase (NSE) and non-neuronal enolase (NNE) in the rat cerebellum at various postnatal developmental stages. Synthetic 45 meric oligonucleotides corresponding to partial sequences of the non-coding region of rat NSE or NNE **mRNA** were 35S-labeled to approximately the same specific activity and used as hybridization probes. On examination of the adult rat cerebellum, both NSE and NNE signals were detected in all identified and presumed neurons which included Purkinje cells, internal granule cells and presumed stellate/basket cells in the cerebellar cortex and neurons of the dentate nucleus. Examination of the cerebellum during postnatal development also revealed coexistence of NSE and NNE signals in these neurons from early stages. During development, both signals coincidentally increased in Purkinje cells and neurons of the dentate nucleus, while only NSE signals showed a gradual increase in the internal granule cells in which NNE signals remained at the same level from early postnatal to adult stages. The external granule cells showed NNE signals until postnatal day 7 but thereafter the signals became less distinct, especially in cells of the inner zone of the external granule cell layer. Thus, it was shown that NSE and NNE were commonly coexpressed at the **mRNA** level in various neurons of the cerebellum except for very undifferentiated external granule cells which expressed only NNE **mRNA**.

L4 ANSWER 12 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 1992:382856 BIOSIS

DOCUMENT NUMBER: PREV199243049806; BR43:49806

TITLE: THE **LOCALIZATION** OF PEROXISOMAL ACYL-COA OXIDASE **MRNA** BY **IN-SITU HYBRIDIZATION** METHOD WITH LIGHT AND ELECTRON MICROSCOPIC RADIOAUTOGRAPHY.

AUTHOR(S): **NAGATA T** [Reprint author]; USUDA N

CORPORATE SOURCE: DEP ANATOMY CELL BIOL, SHINSHU UNIV SCH MED, MATSUMOTO, JPN

SOURCE: Journal of Histochemistry and Cytochemistry, (1992) Vol. 40, No. 4, pp. 591.

Meeting Info.: 43RD ANNUAL MEETING OF THE HISTOCHEMICAL SOCIETY, BETHESDA, MARYLAND, USA, MAY 15-16, 1992. J HISTOCHEM CYTOCHEM.

CODEN: JHCYAS. ISSN: 0022-1554.

DOCUMENT TYPE: Conference; (Meeting)

FILE SEGMENT: BR

LANGUAGE: ENGLISH

ENTRY DATE: Entered STN: 17 Aug 1992
Last Updated on STN: 1 Oct 1992

L4 ANSWER 13 OF 14 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN

ACCESSION NUMBER: 91:202640 SCISEARCH

WEST Search History

DATE: Monday, March 01, 2004

Hide?	Set Name	Query	Hit Count
<i>DB=PGPB,USPT,USOC,EPAB,DWPI; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L1	screen\$ near genes	13
<input type="checkbox"/>	L2	screen\$ near gene	5350
<input type="checkbox"/>	L3	(screen\$ near gene) same (in situ hybridization)	4
<input type="checkbox"/>	L4	L2 same hybridization	906
<input type="checkbox"/>	L5	L4 and (probe same (mRNA or express\$ seqenc\$ tag or EST))	494
<input type="checkbox"/>	L6	L5 and (product near (gene expression))	0
<input type="checkbox"/>	L7	L6 and (product same (gene expression))	0
<input type="checkbox"/>	L8	L5 and (product same (gene expression))	227
<input type="checkbox"/>	L9	L8 and (DNA chip or DNA microarray or microarray or microchip or chip)	53
<input type="checkbox"/>	L10	L9 and localization	35
<input type="checkbox"/>	L11	(probe same mRNA) same (in situ hybridization)	674
<input type="checkbox"/>	L12	L11 and (EST or exprpress\$ sequence tag or mRNA)	674
<input type="checkbox"/>	L13	L12 and (Localization same mRNA)	307
<input type="checkbox"/>	L14	L13 and (different\$ tissue or different cell)	93
<input type="checkbox"/>	L15	L14 and (DNA chip or DNA microarray or microarray or microchip or chip)	42
<input type="checkbox"/>	L16	(localization near MRNA) or (localization near (express\$ sequence tag or EST))	320
<input type="checkbox"/>	L17	L16 and (in situ hybridization)	133
<input type="checkbox"/>	L18	L17 and (probe near (specifically hybriz\$) near mRNA)	0
<input type="checkbox"/>	L19	L17 and (probe near mRNA)	28
<i>DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L20	screening near genes	1700
<input type="checkbox"/>	L21	L20 same in situ hybridization	0
<input type="checkbox"/>	L22	L20 and in situ hybridization	99
<input type="checkbox"/>	L23	L22 and (mRNA localization)	0
<input type="checkbox"/>	L24	L22 and (gene near unknown near function)	1
<input type="checkbox"/>	L25	L22 and (DNA chip or DNA microarray or microarray or microchip or chip)	44

END OF SEARCH HISTORY

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(FILE 'HOME' ENTERED AT 15:54:57 ON 01 MAR 2004)

FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT' ENTERED
AT 15:55:33 ON 01 MAR 2004

L1 31061 S ASAI S?/AU OR NAGATA T?/AU OR TAKAHASHI Y?/AU OR ISHIKAWA K?/
L2 266 S L1 AND IN SITU HYBRIDIZATION
L3 29 S L2 AND (LOCALIZATION AND MRNA)
L4 14 DUP REM L3 (15 DUPLICATES REMOVED)
L5 59 S IN SITU HYBRIDIZATION
L6 15258 S INSITU HYBRIDIZATION
L7 257067 S IN SITU HYBRIDIZATION
L8 1449 S (L6 OR L7) AND (SCREEN### (5A) GENE#)
L9 2 S L8 AND (LOCALIZATION (3A) MRNA)
L10 73 S L8 AND (LOCALIZATION AND MRNA)
L11 7 S L10 AND (DNA CHIP OR MICROCHIP OR MICROARRAY OR DNA MICROARRA
L12 4 DUP REM L11 (3 DUPLICATES REMOVED)
L13 387 S L8 AND MRNA
L14 28 S L13 AND (DNA CHIP OR MICROCHIP OR MICROARRA OR CHIP OR ARRAY)
L15 20 DUP REM L14 (8 DUPLICATES REMOVED)
L16 38 DUP REM L10 (35 DUPLICATES REMOVED)
L17 383 S L13 AND L7
L18 63 S L17 AND PROBE
L19 42 DUP REM L18 (21 DUPLICATES REMOVED)
L20 12 S L19 AND LOCALIZ?
L21 12 DUP REM L20 (0 DUPLICATES REMOVED)

=>

in the brain, such as subtractive hybridization, mRNA differential display, and cDNA microarray technology, outlining advantages and disadvantages of these methods. Finally, we summarize our initial results of a systematic screening of gene expression in the rat brain across behavioural states using mRNA differential display and cDNA microarray technology. The expression pattern of approximately 7000 genes was analysed in the cerebral cortex of rats after 3 h of spontaneous sleep, 3 h of spontaneous waking, or 3 h of sleep deprivation. While the majority of transcripts were expressed at the same level among these three conditions, 14 mRNAs were modulated by sleep and waking. Six transcripts, four more expressed in waking and two more expressed in sleep, corresponded to novel genes. The eight known transcripts were all expressed at higher levels in waking than in sleep and included transcription factors and mitochondrial genes. A possible role for these known transcripts in mediating neural plasticity during waking is discussed.

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(FILE 'HOME' ENTERED AT 15:54:57 ON 01 MAR 2004)

FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT' ENTERED AT 15:55:33 ON 01 MAR 2004

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L1      31061 S ASAI S?/AU OR NAGATA T?/AU OR TAKAHASHI Y?/AU OR ISHIKAWA K?/
L2      266 S L1 AND IN SITU HYBRIDIZATION
L3      29 S L2 AND (LOCALIZATION AND MRNA)
L4      14 DUP REM L3 (15 DUPLICATES REMOVED)
L5      59 S IN SITU HYBRIDIZATION
L6      15258 S INSITU HYBRIDIZATION
L7      257067 S IN SITU HYBRIDIZATION
L8      1449 S (L6 OR L7) AND (SCREEN### (5A) GENE#)
L9      2 S L8 AND (LOCALIZATION (3A) MRNA)
L10     73 S L8 AND (LOCALIZATION AND MRNA)
L11     7 S L10 AND (DNA CHIP OR MICROCHIP OR MICROARRAY OR DNA MICROARRA
L12     4 DUP REM L11 (3 DUPLICATES REMOVED)
L13     387 S L8 AND MRNA
L14     28 S L13 AND (DNA CHIP OR MICROCHIP OR MICROARRA OR CHIP OR ARRAY)
L15     20 DUP REM L14 (8 DUPLICATES REMOVED)
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PROCESSING COMPLETED FOR L10

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L16     38 DUP REM L10 (35 DUPLICATES REMOVED)
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L16 ANSWER 1 OF 38 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN

ACCESSION NUMBER: 2003:657176 SCISEARCH

THE GENUINE ARTICLE: 704DX

TITLE: Identification of upregulated SCG10 mRNA expression associated with late-phase long-term potentiation in the rat hippocampal Schaffer-CA1 pathway in vivo

AUTHOR: Peng H X (Reprint); Derrick B E; Martinez J L

CORPORATE SOURCE: Univ Texas, Dept Biol, Cajal Neurosci Inst, 6900 N Loop 1604 W, San Antonio, TX 78249 USA (Reprint); Univ Texas, Dept Biol, Cajal Neurosci Inst, San Antonio, TX 78249 USA

COUNTRY OF AUTHOR: USA

SOURCE: JOURNAL OF NEUROSCIENCE, (23 JUL 2003) Vol. 23, No. 16, pp. 6617-6626.

Publisher: SOC NEUROSCIENCE, 11 DUPONT CIRCLE, NW, STE 500, WASHINGTON, DC 20036 USA.

ISSN: 0270-6474.

DOCUMENT TYPE: Article; Journal

LANGUAGE: English
REFERENCE COUNT: 77

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The maintenance of long-term potentiation (LTP) depends on alteration of **gene** transcription. By **screening** a subtracted cDNA library that is enriched in upregulated transcripts in rat hippocampus 3 hr after Schaffer-CA1 LTP induction in vivo, we identified a neural growth-associated protein SCG10 (superior cervical ganglia clone 10) gene. The semiquantitative reverse transcription-PCR and Northern blot experiments confirmed that SCG10 **mRNA** levels were elevated in tetanized rat hippocampi compared with those of sham controls that received only low-frequency stimulation. Both 1 and 2 kb forms of SCG10 mRNAs contributed to the increased expression. Using a riboprobe with a sequence specific to the 3'-untranslated region of rat SCG10 **mRNA**, in **situ hybridization** further revealed a significant increase of the SCG10 **mRNA** 2 kb form in the ipsilateral CA3 and CA1 regions of LTP animals. In addition, we systemically injected the competitive NMDA receptor antagonist D,L-3[(+/-)-2-carboxypiperazine-4-yl]-propyl-1-phosphonic acid (CPP) to determine whether the alteration of SCG10 expression depends on NMDA receptor activation or tetanus alone. Administration of CPP 1 hr before tetanus completely blocked LTP induction and the increase of SCG10 **mRNA** levels. Thus, these results suggest that the transcription of SCG10 in vivo is regulated by long-lasting synaptic activity and may contribute to the maintenance of long-term synaptic plasticity via a presynaptic remodeling mechanism.

L16 ANSWER 2 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 2003453051 EMBASE
TITLE: Distribution of α - and γ -synucleins in the adult rat brain and their modification by high-dose cocaine treatment.
AUTHOR: Brenz Verca M.S.; Bahi A.; Boyer F.; Wagner G.C.; Dreyer J.-L.
CORPORATE SOURCE: Dr. J.-L. Dreyer, Institute of Biochemistry, University of Fribourg, CH-1700 Fribourg, Germany. jean-luc.dreyer@unifr.ch
SOURCE: European Journal of Neuroscience, (2003) 18/7 (1923-1938).
Refs: 55
ISSN: 0953-816X CODEN: EJONEI
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 008 Neurology and Neurosurgery
037 Drug Literature Index
052 Toxicology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Synucleins have attracted much attention because of their involvement in several neurodegenerative disorders. In a **screening** for **genes** differentially expressed after high-dose cocaine exposure, we found γ -synuclein as a major upregulated candidate in the tegmentum. Overexpression of both α - and γ -synuclein after drug treatment was confirmed by means of microarrays, yielding an increase in the hippocampus, the striatum and the tegmentum (2.65 x, 1.96 x and 3.5 x, respectively, for α -synuclein vs. 2.7 x, 1.96 x and 7.16 x for γ -synuclein), but no change in the nucleus accumbens. Investigation of the distribution of **mRNA** (by in **situ hybridization**) and of the proteins (by immunocytochemistry) shows in both cases a clearly distinct pattern of expression for α - and γ -synuclein. α -synuclein displays a very characteristic distribution, confined to specific nuclei, whereas γ -synuclein is more widely expressed throughout the brain. **mRNA** of both α - and γ -synucleins display a complementary pattern of expression all over the cortex. In contrast to γ -synuclein,

α -synuclein is neuronal, being only found in NeuN-expressing cells, and is expressed in the basal ganglia (faintly) and in the substantia nigra compacta where it is highly correlated with tyrosine hydroxylase. Immunocytochemistry shows that γ -synuclein generally colocalizes with glial fibrillary acidic protein-expressing cells and is abundant in the red nucleus, the substantia nigra reticulata and the anterior commissure, while γ -synuclein mRNA labels the matrix compartments of the caudate-putamen. The role of synucleins in relation to cocaine-induced plasticity or neurotoxicity is discussed.

L16 ANSWER 3 OF 38 MEDLINE on STN DUPLICATE 1
 ACCESSION NUMBER: 2003239107 MEDLINE
 DOCUMENT NUMBER: PubMed ID: 12761244
 TITLE: AngRem104, an angiotensin II-induced novel upregulated gene in human mesangial cells, is potentially involved in the regulation of fibronectin expression.
 AUTHOR: Liang Xiubin; Zhang Hong; Zhou Anyu; Wang Haiyan
 CORPORATE SOURCE: Renal Division of Peking University First Hospital, Institute of Nephrology, Peking University, Beijing, China.
 SOURCE: Journal of the American Society of Nephrology : JASN, (2003 Jun) 14 (6) 1443-51.
 Journal code: 9013836. ISSN: 1046-6673.
 PUB. COUNTRY: United States
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF367870
 ENTRY MONTH: 200308
 ENTRY DATE: Entered STN: 20030523
 Last Updated on STN: 20030821
 Entered Medline: 20030820

AB Accumulation of extracellular matrix (ECM) in the glomerular mesangium is a common feature of many progressive renal diseases. Angiotensin II (AngII) plays important roles in the proliferation of glomerular mesangial cells (MC) as well as the synthesis of ECM such as fibronectin (FN) and collagens. However, the precise molecular signals responsible for these effects are unknown. To explore possible molecule mechanism of ECM accumulation related to AngII, suppression subtractive hybridization (SSH) was performed to **screen** and identify upregulated **genes** induced by AngII in cultured human MC. A novel gene, AngRem104 (GenBank accession number, AF367870), was isolated. The full-length cDNA of AngRem104 is 1690 bp, and it contains a 1041-bp open reading frame (ORF) encoding 347 amino acid residues with a predicted molecular mass of 37.2 kD. AngRem104 widely expressed in human heart, placenta, liver, muscle, kidney, and pancreas. Moreover, AngRem104 was found in human glomeruli and tubule by **in situ hybridization**. In human MC, the upregulation of AngRem104 induced by AngII was time-dependent, and it was dose-dependently blocked by AngII type 1 receptor antagonist (AT1RA), Losartan. The subcellular **localization** detected by AngRem104-pEGFP fusion protein revealed that AngRem104 was a nuclear protein. Interestingly, when AngRem104 was overexpressed by transfection of its sense construct, cDNA Microarray showed that two of the ECM-related genes, i.e., human mRNA for FN and integrin-beta-1 (FN receptor), dramatically upregulated their expressions. Furthermore, AngRem104 could regulate the expression of FN induced by AngII, which were detected by RT-PCR and quantitative real-time PCR, when AngRem104 was overexpressed. It is concluded that AngRem104 is a novel human gene potentially involved in the regulation of FN induced by AngII in human MC. These findings may provide new insights into mechanisms of glomerular sclerosis associated with AngII.

L16 ANSWER 4 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
 on STN
 ACCESSION NUMBER: 2003174663 EMBASE

TITLE: Angiogenic protein Cyr61 is expressed by podocytes in anti-Thy-1 glomerulonephritis.

AUTHOR: Sawai K.; Mori K.; Mukoyama M.; Sugawara A.; Suganami T.; Koshikawa M.; Yahata K.; Makino H.; Nagae T.; Fujinaga Y.; Yokoi H.; Yoshioka T.; Yoshimoto A.; Tanaka I.; Nakao K.

CORPORATE SOURCE: Dr. K. Mori, Department of Medicine, Kyoto Univ. Grad. School of Medicine, 54 Shogoin Kawahara-cho, Sakyo-ku, Kyoto 606-8507, Japan. keyem@kuhp.kyoto-u.ac.jp

SOURCE: Journal of the American Society of Nephrology, (1 May 2003) 14/5 (1154-1163).
Refs: 42
ISSN: 1046-6673 CODEN: JASNEU

COUNTRY: United States

DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 028 Urology and Nephrology
029 Clinical Biochemistry

LANGUAGE: English

SUMMARY LANGUAGE: English

AB Dynamic recovery of glomerular structure occurs after severe glomerular damage in anti-Thy-1 glomerulonephritis (Thy-1 GN), but its mechanism remains to be investigated. To identify candidate **genes** possibly involved in glomerular reconstruction, **screening** was performed for **genes** that are specifically expressed by podocytes and are upregulated in glomeruli of Thy-1 GN. Among them, cysteine-rich protein 61 (Cyr61 or CCN1), a soluble angiogenic protein belonging to the CCN family, was identified. By Northern blot analysis, Cyr61 **mRNA** was markedly upregulated in glomeruli of Thy-1 GN from day 3 through day 7, when mesangial cell migration was most prominent. By **in situ hybridization** and immunohistochemistry, Cyr61 **mRNA** and protein were expressed by proximal straight tubules and afferent and efferent arterioles in normal rat kidneys and were intensely upregulated at podocytes in Thy-1 GN. Platelet-derived growth factor-BB (PDGF-BB) and transforming growth factor- β 1 (TGF- β 1), of which the gene expression in the glomeruli of Thy-1 GN was upregulated in similar time course as Cyr61, induced Cyr61 **mRNA** expression in cultured podocytes. Furthermore, supernatant of Cyr61-overexpressing cells inhibited PDGF-induced mesangial cell migration. In conclusion, it is shown that Cyr61 is strongly upregulated at podocytes in Thy-1 GN possibly by PDGF and TGF- β . Cyr61 may be involved in glomerular remodeling as a factor secreted from podocytes to inhibit mesangial cell migration.

L16 ANSWER 5 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 2003091098 EMBASE

TITLE: Molecular characterization and expression of porcine bone morphogenetic protein receptor-IB in the uterus of cyclic and pregnant gilts.

AUTHOR: Kim J.G.; Song J.H.; Vallet J.L.; Rohrer G.A.; Johnson G.A.; Joyce M.M.; Christenson R.K.

CORPORATE SOURCE: R.K. Christenson, USDA, ARS, U.S. Meat Animal Research Center, P.O. Box 166, Clay Center, NE 68933-0166, United States. christenson@email.marc.usda.gov

SOURCE: Biology of Reproduction, (1 Mar 2003) 68/3 (735-743).
Refs: 41
ISSN: 0006-3363 CODEN: BIREBV

COUNTRY: United States

DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 021 Developmental Biology and Teratology
029 Clinical Biochemistry

LANGUAGE: English

SUMMARY LANGUAGE: English

AB Previous gene mapping analyses revealed a quantitative trait locus for uterine capacity on chromosome 8. Comparison of porcine and human genetic maps suggests that the bone morphogenetic protein receptor IB (BMPR-IB)

gene may be located near this region. The objectives of this study were to 1) clone the full coding region for BMPR-IB, 2) examine BMPR-IB gene expression by the endometrium and its cellular **localization** in cyclic and pregnant gilts, and 3) map the BMPR-IB **gene**. By iterative **screening** of an expressed sequence tag library, we obtained a 3559-base pair cDNA clone including the full coding region of BMPR-IB. Endometrial BMPR-IB **mRNA** expression of White composite gilts was determined by Northern blotting in Days 10, 13, and 15 cyclic and Days 10, 13, 15, 20, 30, and 40 pregnant gilts. In cyclic gilts, endometrial BMPR-IB **mRNA** expression was elevated on Days 13 and 15 ($P < 0.01$) compared with Day 10. Expression of BMPR-IB **mRNA** was localized in both luminal and glandular epithelium on Day 15. However, in pregnant gilts, BMPR-IB **mRNA** expression was not significantly different in the endometrium from Day 10 to Day 20, and it was significantly decreased on Days 30 and 40 ($P = 0.011$). The BMPR-IB gene was mapped to 108 cM on chromosome 8. These findings show that BMPR-IB **mRNA** expression is regulated differently in cyclic and pregnant gilts; this pattern of gene expression may be important for endometrial function during the luteal phase of the estrous cycle as compared with early pregnancy.

L16 ANSWER 6 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN DUPLICATE 2

ACCESSION NUMBER: 2003181324 EMBASE
TITLE: Erol-L, an ischemia-inducible gene from rat brain with homology to global ischemia-induced gene 11 (Giig11), is localized to neuronal dendrites by a dispersed identifier (ID) element-dependent mechanism.
AUTHOR: Chen D.; Jin K.; Kawaguchi K.; Nakayama M.; Zhou X.; Xiong Z.; Zhou A.; Mao X.O.; Greenberg D.A.; Graham S.H.; Simon R.P.
CORPORATE SOURCE: Dr. R.P. Simon, Robert S. Dow Neurobio. Laboratories, Legacy Research, 1225 NE 2nd Avenue, Portland, OR 97232, United States. rsimon@DowNeurobiology.org
SOURCE: Journal of Neurochemistry, (2003) 85/3 (670-679).
Refs: 50
ISSN: 0022-3042 CODEN: JONRA
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 008 Neurology and Neurosurgery
022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Many changes in neuronal gene expression occur in response to ischemia, and these may play a role in determining the fate of ischemic neurons. To identify genes induced in the rat brain following cerebral ischemia, a strategy was used that combines subtractive hybridization and differential **screening**. Among the **genes** identified was one referred to as global ischemia-inducible gene 11 (Giig11). Sequence analysis indicated that Giig11 exhibited 97% and 91% identity to the known Erol-L (*S. cerevisiae* erol-like oxidoreductase) of mouse and human origin, which is involved in oxidative endoplasmic reticulum protein folding. Rat Erol-L/Giig11 also contains a 107-bp sequence that is nearly identical (> 95%) to the known dispersed repetitive identifier (ID), but which is lacking in mouse and human Erol-L. Northern blotting showed that expression of the ID element and Erol-L/Giig11 **mRNA** increased after global cerebral ischemia. In **situ hybridization** demonstrated increased expression of Erol-L/Giig11 in the brain following ischemic injury, with the highest levels in the vulnerable hippocampal CA1 pyramidal neurons. Transfection of cultured primary hippocampal neurons with a plasmid containing green fluorescent protein (gfp) and Erol-L/Giig11 cDNA (with and without the ID element) produced a gfp-Erol-L/Giig11 fusion protein, and more fusion protein was localized into dendrites in the presence of the ID element, suggesting that the ID

element promotes Ero1-L/Giig11 protein **localization** to dendrites. Therefore, Ero-1L/Giig11 may have a role in ischemia-induced neuronal repair or survival mechanisms directed at counteracting abnormalities in protein folding, maturation and distribution.

L16 ANSWER 7 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 2003330687 EMBASE
TITLE: Global gene profiling analysis of mouse uterus during the oestrous cycle.
AUTHOR: Tan Y.F.; Li F.X.; Piao Y.S.; Sun X.Y.; Wang Y.L.
CORPORATE SOURCE: Y.L. Wang, State Key Lab. Reproductive Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing 100080, China. wangyl@panda.ioz.ac.cn
SOURCE: Reproduction, (1 Aug 2003) 126/2 (171-182).
Refs: 53
ISSN: 1470-1626 CODEN: RCUKBS
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 003 Endocrinology
021 Developmental Biology and Teratology
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Many genes related to the cyclic changes of the uterus during the oestrous cycle have been identified using a one-by-one approach. In the present study, cDNA microarray technology was applied to investigate the global profile of gene expression of mouse uterus at the oestrous and dioestrous stages. At a certain stage of the oestrous cycle, the uteri of mature CD-1 mice (n = 10) were removed, pooled and snap-frozen in liquid nitrogen. Total RNA was extracted to synthesize cDNA probes for microarray assay. By **screening** 8192 mouse **genes** and expressed sequence tags (ESTs), 51 upregulated and 51 downregulated genes were identified in oestrous uterus, of which 62 are well characterized and 40 are ESTs. The known genes were assigned to various gene categories according to their main function. The microarray was performed three times with three independent sets of uterine tissue pools. The results of northern blot analysis for small proline-rich protein 2 (Sprr2), 17 β -hydroxysteroid dehydrogenase type 2 (17 β HSD-2), high mobility group 2 (Hmg2), mitotic checkpoint component 2 (Mad2) and an EST AW555366 **mRNA** were consistent with that of microarray analysis. In **situ hybridization** was performed to localize the transcript of the EST AW555366. Most of the upregulated genes encode secreted immune-related proteins, proteinases and their inhibitors, indicating their potential involvement in sperm viability as well as capacitation. The downregulated genes mainly encode cell cycle-related factors, implying the active proliferation of uterus at dioestrus.

L16 ANSWER 8 OF 38 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 2003:310511 BIOSIS
DOCUMENT NUMBER: PREV200300310511
TITLE: Cloning and characterization of SLP3: A novel member of the stomatin family expressed by olfactory receptor neurons.
AUTHOR(S): Goldstein, Bradley J.; Kulaga, Heather M.; Reed, Randall R. [Reprint Author]
CORPORATE SOURCE: Department of Molecular Biology and Genetics, Howard Hughes Medical Institute, Johns Hopkins University School of Medicine, 725 N. Wolfe St., 800 PCTB, Baltimore, MD, 21205, USA
rreed@jhmi.edu
SOURCE: JARO Journal of the Association for Research in Otolaryngology, (March 2003) Vol. 4, No. 1, pp. 74-82.
print.
ISSN: 1525-3961 (ISSN print).

DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 2 Jul 2003
Last Updated on STN: 2 Jul 2003

AB The detection of odorants with high sensitivity and specificity utilizes specialized transduction proteins that may be assembled into complexes to afford enhanced speed and efficiency in olfactory neurons. We have used a differential cDNA **screening** technique to identify novel **gene** products that display restricted expression within the olfactory epithelium. Here we report the characterization of an olfactory neuronal protein, SLP3, which shares extensive homology with the stomatin family of membrane proteins. Other stomatin family members have been implicated in specific interactions with ion channels and G protein-coupled receptors. The pattern of SLP3 **mRNA** expression during embryonic development and the subcellular **localization** of the SLP3 protein in mature olfactory neurons observed here is consistent with a specific role for this protein in the assembly, translocation, or function of the odorant transduction complex in olfactory neurons.

L16 ANSWER 9 OF 38 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN

ACCESSION NUMBER: 2002-14126 BIOTECHDS

TITLE: Novel peptide designated as human kinase useful as target for diagnosing a disease or predisposition to the disease mediated by the peptide;
vector-mediated gene transfer, expression in host cell and antibody for recombinant protein production, drug **screening** and **gene** therapy

AUTHOR: BEASLEY E M; WEI M; BONAZZI V R; SANDERS R; DI FRANCESCO V

PATENT ASSIGNEE: PE CORP NY

PATENT INFO: WO 2002024920 28 Mar 2002

APPLICATION INFO: WO 2000-US29161 19 Sep 2000

PRIORITY INFO: US 2000-729995 6 Dec 2000

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2002-404955 [43]

AN 2002-14126 BIOTECHDS

AB DERWENT ABSTRACT:

NOVELTY - An isolated peptide designated human kinase (HK) consisting or comprising of an amino acids sequence (S1) containing 505 amino acids fully defined in the specification, its allelic variant, ortholog or fragment, is new.

DETAILED DESCRIPTION - HK comprises (S1), its ortholog, variant or fragment, each comprising (S1), where the variant or ortholog is encoded by a nucleic acid molecule that hybridizes under stringent conditions to the opposite strand of the nucleic acid molecule comprising a sequence (S2) of 2190 or 29629 base pairs fully defined in the specification, or the fragment comprises 10 contiguous amino acids. INDEPENDENT CLAIMS are included for the following: (1) an isolated antibody (Ab) that binds to HK; (2) an isolated nucleic acid molecule (NA) consisting and/or comprising a nucleotide sequence from the same which encodes (S1), its variant ortholog, and fragment, each encoded by (S1) where the variant and ortholog are encoded by (S2), the fragment comprising 10 contiguous amino acids and the complement of the nucleotide sequence; (3) a gene chip comprising NA; (4) a transgenic non-human animal (NHA) comprising NA; (5) a nucleic acid vector (V) comprising NA; (6) a host cell (HC) containing (V); (7) producing HK; (8) a pharmaceutical composition (PC) comprising an agent identified by contacting HK with it and assaying the mixture to determine whether a complex is formed with the agent bound to the peptide; (9) an isolated human kinase peptide having a sequence 70% identical to (S1); (10) an isolated nucleic acid molecule encoding a human kinase peptide having 80% homology with (S2); (11) detecting the presence of HK in a sample involving contacting the sample with a detection agent that specifically allows detection of the presence of HK in the sample and then detecting the presence of HK; and (12) detecting

the presence of NA in a sample involving contacting the sample with an oligonucleotide that hybridizes to NA under stringent conditions and determining whether oligonucleotide binds to NA in the sample.

WIDER DISCLOSURE - The following are disclosed: (1) kits for using antibodies to detect the presence of a protein in a biological sample, detecting the presence of kinase nucleic acid in a biological sample; and (2) nucleic acid detection kits, such as arrays or microarrays of nucleic acid molecules that are based on the sequence information provided in (S2).

BIOTECHNOLOGY - Preparation: Producing HK involves introducing a nucleotide sequence encoding (S1) into HC, and culturing HC under conditions in which the peptides (HK) are expressed from the nucleotide sequence (claimed). Preferred Peptide: HK shares 90% homology with (S1). Preferred Nucleic Acid: NA shares 90% homology with (S2).

ACTIVITY - None given.

MECHANISM OF ACTION - Kinase modulator. No supporting data is given.

USE - HK is useful for identifying a modulator of it, by contacting HK with an agent and determining if the agent has modulated the function, expression or activity of HK, where the agent is administered to HC comprising an expression vector that expresses HK. HK is also useful for identifying an agent that binds to any of the peptides involving contacting HK with an agent and assaying the contacted mixture to determine whether a complex is formed with the agent bound to HK. PC is useful for treating a disease, or condition mediated by HK (claimed). HK is useful to screen a compound for the ability to stimulate or inhibit interaction between HK and molecule that normally interacts with HK. HK is useful as bait proteins in a 2 or 3 hybrid assays to identify other proteins, which bind or interact with HK and are involved in HK activity. HK is also useful to provide a target for diagnosing a disease or predisposition to disease mediated by HK and also useful in pharmacogenetic analysis. HK is also useful for treating a disorder characterized by absence of inappropriate or unwanted expression of HK, also as an immunogen to raise Ab by administering HK to a mammalian organism e.g. rat, rabbit or mouse. Ab is useful to isolate HK by affinity chromatography or immuno precipitation and also to detect protein in situ in vitro or in a cell lysate or supernatant in order to evaluate the abundance and pattern of expression. Ab is also useful to assess normal and aberrant subcellular **localization** of cells in various tissues in an organism. Ab is also useful in pharmacogenomic analysis and also useful as diagnostic tools as an immunological marker for aberrant protein analyzed by electrophoretic mobility, isoelectric point, tryptic peptide digest and other physical assays. Ab is further useful in tissue typing where a specific protein has been correlated with expression in specific tissue, antibodies that are specific for this protein which can be useful to identify a tissue type. NA is useful as a hybridization probes for **mRNA**, transcript/cDNA and genomic DNA to isolate full length cDNA and genomic clones encoding the peptide and to isolate cDNA and genomic clones that corresponds to variants producing the same or related peptides, to synthesize antisense molecules of desired length and sequence and also useful as probes for determining the chromosomal positions of it by means of in **situ hybridization** methods. NA is useful in making vectors containing the gene regions of NA, for designing ribozymes corresponding to all or a part of **mRNA** produced from NA, for constructing HC and also for constructing transgenic animals expressing NA and peptides. NA is also useful as hybridization probes for determining the presence level, form and distribution of NA expression, for monitoring the effectiveness of modulating compounds on the expression or activity of HK gene in clinical trials or in treatment regimen and also useful as antisense constructs to control kinase gene expression in cells, tissues and organisms. HC is useful for HK production and also useful for conducting cell-based assays involving the HK or its fragments. Recombinant HC expressing a native HK is useful for assaying compounds that stimulate or inhibit HK function. HC are also useful for identifying HK mutants in which these functions

are affected. Genetically engineered HC are useful to produce NHA, e.g. rodent such as rat or mouse in which one or more of the cells of the animal include a transgene.

EXAMPLE - None given. (90 pages)

L16 ANSWER 10 OF 38 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN

ACCESSION NUMBER: 2003-16287 BIOTECHDS

TITLE: **Screening** of a **gene**, and monitoring of
gene expression comprises in **situ**
hybridization techniques;
gene expression analysis in cerebral anemia mouse animal
model

PATENT ASSIGNEE: UNIV NIPPON

PATENT INFO: JP 2002306174 22 Oct 2002

APPLICATION INFO: JP 2001-112367 11 Apr 2001

PRIORITY INFO: JP 2001-112367 11 Apr 2001; JP 2001-112367 11 Apr 2001

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

OTHER SOURCE: WPI: 2003-423960 [40]

AN 2003-16287 BIOTECHDS

AB DERWENT ABSTRACT:

NOVELTY - **Screening** a **gene** in which a probe
hybridizing specifically with an **mRNA** and/or an expression gene
sequence fragment, which are expression products of a gene used to carry
out an in **situ hybridization** of a biotissue or a cell
sample, and to investigate **localization** of **mRNA**
and/or expression gene sequence fragment in tissue or cell.

DETAILED DESCRIPTION - A method for monitoring gene expression in
which a tissue or a cell sample are respectively collected from a living
body before and after a phenomenon occurs, and the samples are in situ
hybridized by using the above probe to investigate **localization**
of said **mRNA** and/or expression gene sequence fragment in said
tissue or said cell.

USE - The method is used for **screening** a **gene**
and monitoring **gene** expression.

EXAMPLE - Both side total carotid arteries of mature mice were
ligated for 20 minutes to interrupt blood current and to give cerebral
anemia models. The blood current was entrestored, the mice were killed
periodically and the hippocampi were taken and the gene expression was
analyzed. (22 pages)

=> d l16 ibib abs 11-20

L16 ANSWER 11 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 2002299578 EMBASE

TITLE: NATH, a novel gene overexpressed in papillary thyroid
carcinomas.

AUTHOR: Fluge O.; Bruland O.; Akslen L.A.; Varhaug J.E.; Lillehaug
J.R.

CORPORATE SOURCE: O. Fluge, Department of Molecular Biology, University of
Bergen, Thormoohlens gt. 55, N-5020 Bergen, Norway.
oystein.fluge@mbi.uib.no

SOURCE: Oncogene, (1 Aug 2002) 21/33 (5056-5068).
Refs: 44

ISSN: 0950-9232 CODEN: ONCNES

COUNTRY: United Kingdom

DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 003 Endocrinology
016 Cancer
022 Human Genetics

LANGUAGE: English

SUMMARY LANGUAGE: English

AB In this study a replica cDNA **screening** (RCS) approach to identify **genes** differentially expressed in papillary thyroid carcinomas (PTC) was used, as compared to non-neoplastic thyroid tissues. RCS is based on hybridization of radioactively labeled cDNA probes made from the biopsies to replica membranes with 15000 clones from a PTC cDNA library. Among the genes over-expressed in PTC, and especially in clinically aggressive tumors with histologic evidence of poorly differentiated or undifferentiated areas, a novel gene named NATH was found. NATH has two **mRNA** species, 4.6 and 5.8 kb, both harboring the same open reading frame encoding a putative protein of 866 amino acids. The NATH protein is homologous to yeast N-acetyltransferase (NAT)1 and to mouse NARG1 (mNAT1) and contains four tetratricopeptide repeat (TPR) domains, suggesting that NATH may be part of a multiprotein complex. Overlapping RT-PCR fragments from several PTC biopsies confirmed the NATH **mRNA** sequence. Northern blots, semiquantitative RT-PCR experiments, TaqMan real-time RT-PCR experiments, and **in situ hybridization** verified the overexpression of NATH **mRNA** localized to tumor cells in PTC biopsies. NATH was expressed at a low level in most human adult tissues, including the normal thyroid gland. Increased NATH expression was seen especially in a Burkitt lymphoma cell line and in adult human testis. Recombinant in vitro expression showed that NATH protein was located mainly in the cytoplasm, and was present as a single protein band of the expected 105 kDa molecular weight. Heterologous expression of NATH in the papillary carcinoma cell line (NPA) and 293 cells did not alter the cellular proliferation rate. The biological function of NATH remains to be elucidated, but the overexpression in classic PTC and especially in poorly differentiated or undifferentiated components may indicate a function in the progression of papillary thyroid carcinomas.

L16 ANSWER 12 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 2002444770 EMBASE
TITLE: The zebrafish mutant gene chardonnay (cdy) encodes divalent metal transporter 1 (DMT1).
AUTHOR: Donovan A.; Brownlie A.; Dorschner M.O.; Zhou Y.; Pratt S.J.; Paw B.H.; Phillips R.B.; Thisse C.; Thisse B.; Zon L.I.
CORPORATE SOURCE: L.I. Zon, Children's Hospital, 300 Longwood Ave, Boston, MA 02115, United States. zon@enders.tch.harvard.edu
SOURCE: Blood, (15 Dec 2002) 100/13 (4655-4659).
Refs: 43
ISSN: 0006-4971 CODEN: BLOOAW
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 025 Hematology
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Iron is an essential nutrient required for the function of all cells, most notably for the production of hemoglobin in red blood cells. Defects in the mechanisms of iron absorption, storage, or utilization can lead to disorders of iron-limited erythropoiesis or iron overload. In an effort to further understand these processes, we have used the zebrafish as a genetic system to study vertebrate iron metabolism. Here we characterized the phenotype of chardonnay (cdy), a zebrafish mutant with hypochromic, microcytic anemia, and positioned the mutant gene on linkage group 11. The cdy gene was isolated by a functional genomics approach in which we used a combination of expression studies, sequence analyses, and radiation hybrid panel mapping. We identified erythroid-specific genes using a whole embryo **mRNA in situ hybridization screen** and placed these **genes** on the zebrafish genomic map. One of these genes encoded the iron transporter divalent metal transporter 1 (DMT1) and colocalized with the cdy gene. We identified a nonsense

mutation in the cdy allele and demonstrated that, whereas wild-type zebrafish DMT1 protein can transport iron, the truncated protein expressed in cdy mutants is not functional. Our studies further demonstrate the conservation of iron metabolism in vertebrates and suggest the existence of an alternative pathway of intestinal and red blood cell iron uptake.
 .COPYRGT. 2002 by The American Society of Hematology.

L16 ANSWER 13 OF 38 MEDLINE on STN DUPLICATE 3
 ACCESSION NUMBER: 2002197882 MEDLINE
 DOCUMENT NUMBER: PubMed ID: 11895481
 TITLE: Identification of a novel nonlysosomal sulphatase expressed in the floor plate, choroid plexus and cartilage.
 COMMENT: Erratum in: Genes Cells 2002 May;7(5):521-2
 AUTHOR: Ohto Tatsuyuki; Uchida Hiroshi; Yamazaki Hiroshi; Keino-Masu Kazuko; Matsui Akira; Masu Masayuki
 CORPORATE SOURCE: Department of Molecular Neurobiology, Institute of Basic Medical Sciences, University of Tsukuba, Tsukuba, Ibaraki, Japan.
 SOURCE: Genes to cells : devoted to molecular & cellular mechanisms, (2002 Feb) 7 (2) 173-85.
 Journal code: 9607379. ISSN: 1356-9597.
 PUB. COUNTRY: England: United Kingdom
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200207
 ENTRY DATE: Entered STN: 20020405
 Last Updated on STN: 20020816
 Entered Medline: 20020729

AB BACKGROUND: Sulphated glycosaminoglycans (GAGs) attached to proteoglycan core proteins are implicated in cell adhesion, motility and morphogenesis. Variable sulphation patterns, which are thought to be important for regulating proteoglycan function, are generated by sequential reactions during GAG biosynthesis. However, the mechanism by which such diversity is generated remains unclear. RESULTS: A novel sulphatase, designated RsulfFP1, was isolated from rat embryos by **screening** for floor plate specific **genes**. RsulfFP1 and its orthologues show homology with other sulphatases, and have a distinctive hydrophilic insertion. In **situ hybridization** showed that RsulfFP1 **mRNA** is strongly expressed in the floor plate, choroid plexus and cartilage in rat embryos. In vitro transfection experiments revealed that the RsulfFP1 protein is localized to the Golgi apparatus and endoplasmic reticulum, and is not present in the lysosomes. It also appears to be localized on the cell surface. CONCLUSIONS: RsulfFP1, a phylogenetically conserved sulphatase, forms a novel subgroup in the sulphatase family. It shows homology with the lysosomal sulphatases involved in GAG degradation. **Localization** of the RsulfFP1 protein in the Golgi apparatus and on the cell surface, however, suggests that it may play a role in regulating proteoglycan-mediated signalling by the desulphation of GAGs during biosynthesis or after GAGs are presented in the extracellular space.

L16 ANSWER 14 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
 on STN
 ACCESSION NUMBER: 2002318400 EMBASE
 TITLE: Extensive vascularization of developing mouse ovaries revealed by caveolin-1 expression.
 AUTHOR: Bullejos M.; Bowles J.; Koopman P.
 CORPORATE SOURCE: P. Koopman, Institute for Molecular Bioscience, University of Queensland, Brisbane, QLD 4072, Australia.
 p.koopman@imb.uq.edu.au
 SOURCE: Developmental Dynamics, (2002) 225/1 (95-99).
 Refs: 30
 ISSN: 1058-8388 CODEN: DEDYEI
 COUNTRY: United States

DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 001 Anatomy, Anthropology, Embryology and Histology
021 Developmental Biology and Teratology
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Expression **screening** for **genes** preferentially expressed in mouse fetal ovaries relative to testes identified Cav-1 as a candidate female-specific gene. Cav-1 encodes caveolin-1, a component of the cell membrane invaginations known as caveolae, which are involved in lipid regulation and signal transduction. In **situ hybridization** revealed high levels of Cav-1 **mRNA** in developing ovaries, compared with moderate or low levels in testes. Analysis of caveolin-1 protein distribution by immunofluorescence showed this difference to be due to the development of a dense and complex vascular network in the developing ovary. These observations point to a higher degree of differentiation and organization of the early stage mammalian ovary than previously suspected. .COPYRGT. 2002 Wiley-Liss, Inc.

L16 ANSWER 15 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 2002022653 EMBASE
TITLE: Synergistic induction of HSP40 and HSC70 in the mouse hippocampal neurons after cerebral ischemia and ischemic tolerance in gerbil hippocampus.
AUTHOR: Tanaka S.; Kitagawa K.; Ohtsuki T.; Yagita Y.; Takasawa K.; Hori M.; Matsumoto M.
CORPORATE SOURCE: S. Tanaka, Department of Internal Medicine, Osaka University, Graduate School of Medicine, Yamada-oka 2-2, Suita, Osaka 565-0871, Japan. brain@medone.med.osaka-u.ac.jp
SOURCE: Journal of Neuroscience Research, (1 Jan 2002) 67/1 (37-47).
Refs: 43
ISSN: 0360-4012 CODEN: JNREDK
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 005 General Pathology and Pathological Anatomy
008 Neurology and Neurosurgery
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB An ischemia-induced **gene** was **screened** using a differential display technique in mouse transient forebrain ischemia. One of the ischemia-responsive clones was found to encode mouse hsp40. HSP40 has a critical regulatory function in the HSC70 ATPase activity. Expression of hsp40 **mRNA** was low in the nonischemic mouse hippocampus, but it was significantly upregulated 4 hr after ischemia by Northern blot analysis. In **situ hybridization** analysis revealed hsp40 **mRNA** induction in the neuron. HSP40 protein expression was also enhanced in the pyramidal and dentate granular neurons from 2 to 4 days after ischemia. The temporal expression and distribution profile of HSC70 protein was similar to that of HSP40, and both proteins were colocalized in ischemic hippocampal neurons. In the gerbil transient forebrain ischemia model, both HSP40 and HSC70 proteins were expressed strongly in ischemia-resistant CA3 neurons and dentate granule cells 1 day after 5 min ischemia, but were not expressed in vulnerable CA1 neurons. However, both proteins were in parallel expressed in the tolerance-acquired CA1 neurons. Based on the current observation that both HSP40 and HSC70 proteins were synergistically expressed in the ischemia-resistant and tolerance-acquired neurons, cochaperone HSP40 may play a significant role against postischemic neuronal response and lead to cell survival through interaction with simultaneously induced HSC70. .COPYRGT. 2002 Wiley-Liss, Inc.

L16 ANSWER 16 OF 38 MEDLINE on STN DUPLICATE 4
 ACCESSION NUMBER: 2001336597 MEDLINE
 DOCUMENT NUMBER: PubMed ID: 11404423
 TITLE: Neuronal expression of synaptotagmin-related gene 1 is regulated by thyroid hormone during cerebellar development.
 AUTHOR: Potter G B; Facchinetti F; Beaudoin G M 3rd; Thompson C C
 CORPORATE SOURCE: Kennedy Krieger Research Institute and Department of Neuroscience, Johns Hopkins University School of Medicine, Baltimore, Maryland 21205, USA.
 CONTRACT NUMBER: DK46074 (NIDDK)
 SOURCE: Journal of neuroscience : official journal of the Society for Neuroscience, (2001 Jun 15) 21 (12) 4373-80.
 Journal code: 8102140. ISSN: 1529-2401.
 PUB. COUNTRY: United States
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200107
 ENTRY DATE: Entered STN: 20010716
 Last Updated on STN: 20010716
 Entered Medline: 20010712

AB Thyroid hormone (TH) is essential for proper brain development, acting through nuclear receptors that modulate the expression of specific genes in response to hormone binding. In a **screen for genes** regulated by TH in the rat cerebellum, we recently identified a novel gene, synaptotagmin-related gene 1 (Srg1). The Srg1 protein is structurally similar to synaptotagmins, a family of proteins involved in regulating neurotransmission. To elucidate a potential role of Srg1 in brain development, we have investigated the developmental and TH-regulated expression of Srg1 in the neonatal rat brain. We show that expression of both Srg1 RNA and protein is detected only in the brain and specifically in neurons. Srg1 **mRNA** and protein levels increase postnatally, nearing adult levels after the third postnatal week. Neonatal TH deficiency results in a significant reduction and delay in expression of both Srg1 RNA and protein. Using immunohistochemistry, we were able to detect Srg1 protein in numerous brain regions. In the cerebellum, Srg1 protein is localized to the molecular layer, indicating that it is highly expressed in granule cell axons. To further examine Srg1 expression in cerebellar granule cells (CGCs), we used an in vitro cell culture model. In primary cultures of CGCs, Srg1 expression is significantly reduced in the absence of TH. Srg1 **mRNA** is rapidly upregulated in cultured CGCs, suggesting a direct response to TH. Neuronal and TH-regulated expression of Srg1, together with its **localization** to neurites, implicates Srg1 as an important component of the program of gene expression induced by TH in the developing brain.

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 ACCESSION NUMBER: 2001:487314 BIOSIS
 DOCUMENT NUMBER: PREV200100487314
 TITLE: Identification of a differentially expressed transcript in the dorsal root ganglia of galanin knockout mice.
 AUTHOR(S): Kerr, N. C. H. [Reprint author]; Holmes, F. E. [Reprint author]; Wynick, D. [Reprint author]
 CORPORATE SOURCE: URC-Neuroendocrinology, Bristol Royal Infirmary, Bristol, UK
 SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1, pp. 142. print.
 Meeting Info.: 31st Annual Meeting of the Society for Neuroscience. San Diego, California, USA. November 10-15, 2001.
 ISSN: 0190-5295.
 DOCUMENT TYPE: Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)